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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Kai Wang et al.
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For : A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
EXPRESSED IN SKIN CELLS

Examiner :
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Commissioner for Patents
Washington, DC 20231

FILING FORMAL DRAWINGS

Commissioner for Patents:

Enclosed are 15 sheets of formal drawings, Figures 1-5, for filing in the
above-identified application.



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PATENT TRADEMARK OFFICE

Respectfully submitted,

Seed Intellectual Property Law Group PLLC

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Initial assembled sequence
[Strand]

1 AGAAAATACC CACTTTCTCA GGATGATATC AATGGAATCC AGTCCATCTA TGGAGGTCTG
61 CCTAAGGAAC CTGCTAAGCC AAAGGAACCC ACTATACCCC ATGCCTGTGA CCCTGACTTG
121 ACTTTTGACG CTATCACAAC TTTCCGCAGA GAAGTAATGT TCTTTAAAGG CAGGCACCTA
181 TGGAGGATCT ATTATGATAT CACGGATGTT GAGTTTGAAT TAATTGCTTC ATTCTGGCCA
241 TCTCTGCCAG CTGATCTGCA AGCTGCATAC GAGAACCCCA GAGATAAGAT TCTGGTTTTT
301 AAAGATGAAA ACTTCTGGAT GATCAGAGGA TATGCTGTCT TGCCAGATTA TCCCAAATCC
361 ATCCATACAT TAGGTTTTTCC AGGACGTGTG AAGAAAATAG ATGCAGCCGT CTGTGATAAG
421 ACCACAAGAA AAACCTACTT CTTTGTGGGC ATTTGGTGCT GGAGGTTTGA TGAAATGACC
481 CAAACCATGG ACAAAGGGTT CCCGCAGAGA GTGGTAAAC ACTTTCCTGG AATCAGTATC
541 CGTGTGATG CTGCTTTCCA GTACAAAGGA TTCTTCTTTT TCAGCCGTGG ATCAACGCAA
601 TTTGAATACG ACATTAAGAC AAAGAATATT ACCCGAATCA TGAGAACTAA TACTTGTTTT
661 CAATGCAAAG AACCAAAGAA CTCCTCATTT GGTTTTGATA TCAACAAGGA AAAAGCACAT
721 TCAGGAGGCA TAAAGATATT GTATCATAAG AGTTTAAGCT TGTTTATTTT TGGTATTGTT
781 CATTTGCTGA AAAACACTTC TATTTATCAA TAAATTCATA GACCTAAAAT AAA

Fig. 1

gaaagagagg a atg aag cgc ctt ctg ctt ctg ttt ttg ttc ttt ata aca 50
Met Lys Arg Leu Leu Leu Leu Phe Leu Phe Phe Ile Thr
 1 5 10

ttt tct tct gca ttt ccc tta gtc cgg atg atg gaa aat gaa gaa aat 98
Phe Ser Ser Ala Phe Pro Leu Val Arg Met Met Glu Asn Glu Glu Asn
 15 20 25

gtg caa ctg gct cag gca tat ctc aac cag ttc tac tct ctt gaa ata 146
 Val Gln Leu Ala Gln Ala Tyr Leu Asn Gln Phe Tyr Ser Leu Glu Ile
 30 35 40 45

gaa ggg aat cat ctt gtt caa agc aag aat agg agt ctc ata gat gac 194
 Glu Gly Asn His Leu Val Gln Ser Lys Asn Arg Ser Leu Ile Asp Asp
 50 55 60

aaa att cgg gaa atg caa gca ttt ttt gga ttg aca gtg act gga aga 242
 Lys Ile Arg Glu Met Gln Ala Phe Phe Gly Leu Thr Val Thr Gly Arg
 65 70 75

ctg gac tca aac acc ctt gag atc atg aag aca ccc agg tgt ggg gtg 290
 Leu Asp Ser Asn Thr Leu Glu Ile Met Lys Thr Pro Arg Cys Gly Val
 80 85 90

cct gat gtg ggc cag tat ggc tac acc ctc cct ggg tgg aga aaa tac 338
Pro Asp Val Gly Gln Tyr Gly Tyr Thr Leu Pro Gly Trp Arg Lys Tyr
 95 100 105

aac ctc acc tac aga ata ata aac tat act ccg gat atg gca cga gct 386
 Asn Leu Thr Tyr Arg Ile Ile Asn Tyr Thr Pro Asp Met Ala Arg Ala
 110 115 120 125

gct gtg gat gag gct atc caa gaa ggt tta gaa gtg tgg agc aaa gtc 434
 Ala Val Asp Glu Ala Ile Gln Glu Gly Leu Glu Val Trp Ser Lys Val
 130 135 140

act cca cta aaa ttc acc aag att tca aag ggg att gca gac atc atg 482
 Thr Pro Leu Lys Phe Thr Lys Ile Ser Lys Gly Ile Ala Asp Ile Met
 145 150 155

Fig. 2A

att gcc ttt agg act cga gtc cat ggt cgg tgt cct cgc tat ttt gat 530
 Ile Ala Phe Arg Thr Arg Val His Gly Arg Cys Pro Arg Tyr Phe Asp
 160 165 170

ggt ccc ttg gga gtt ctt ggc cat gcc ttt cct cct ggt ccg ggt ctg 578
 Gly Pro Leu Gly Val Leu Gly His Ala Phe Pro Pro Gly Pro Gly Leu
 175 180 185

ggt ggt gac act cat ttt gat gag gat gaa aac tgg acc aag gat gga 626
 Gly Gly Asp Thr His Phe Asp Glu Asp Glu Asn Trp Thr Lys Asp Gly
 190 195 200 205

gca gga ttc aac ttg ttt ctt gtg gct gct cat gaa ttt ggt cat gca 674
 Ala Gly Phe Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ala
 210 215 220

ctg ggg ctc tct cac tcc aat gat caa aca gcc ttg atg ttc cca aat 722
 Leu Gly Leu Ser His Ser Asn Asp Gln Thr Ala Leu Met Phe Pro Asn
 225 230 235

tat gtc tcc ctg gat ccc aga aaa tac cca ctt tct cag gat gat atc 770
 Tyr Val Ser Leu Asp Pro Arg Lys Tyr Pro Leu Ser Gln Asp Asp Ile
 240 245 250

aat gga atc cag tcc atc tat gga ggt ctg cct aag gaa cct gct aag 818
 Asn Gly Ile Gln Ser Ile Tyr Gly Gly Leu Pro Lys Glu Pro Ala Lys
 255 260 265

cca aag gaa ccc act ata ccc cat gcc tgt gac cct gac ttg act ttt 866
 Pro Lys Glu Pro Thr Ile Pro His Ala Cys Asp Pro Asp Leu Thr Phe
 270 275 280 285

gac gct atc aca act ttc cgc aga gaa gta atg ttc ttt aaa ggc agg 914
 Asp Ala Ile Thr Thr Phe Arg Arg Glu Val Met Phe Phe Lys Gly Arg
 290 295 300

cac cta tgg agg atc tat tat gat atc acg gat gtt gag ttt gaa tta 962
 His Leu Trp Arg Ile Tyr Tyr Asp Ile Thr Asp Val Glu Phe Glu Leu
 305 310 315

Fig. 2B

att gct tca ttc tgg cca tct ctg cca gct gat ctg caa gct gca tac 1010
 Ile Ala Ser Phe Trp Pro Ser Leu Pro Ala Asp Leu Gln Ala Ala Tyr
 320 325 330

gag aac ccc aga gat aag att ctg gtt ttt aaa gat gaa aac ttc tgg 1058
 Glu Asn Pro Arg Asp Lys Ile Leu Val Phe Lys Asp Glu Asn Phe Trp
 335 340 345

atg atc aga gga tat gct gtc ttg cca gat tat ccc aaa tcc atc cat 1106
 Met Ile Arg Gly Tyr Ala Val Leu Pro Asp Tyr Pro Lys Ser Ile His
 350 355 360 365

aca tta ggt ttt cca gga cgt gtg aag aaa ata gat gca gcc gtc tgt 1154
 Thr Leu Gly Phe Pro Gly Arg Val Lys Lys Ile Asp Ala Ala Val Cys
 370 375 380

gat aag acc aca aga aaa acc tac ttc ttt gtg ggc att tgg tgc tgg 1202
 Asp Lys Thr Thr Arg Lys Thr Tyr Phe Phe Val Gly Ile Trp Cys Trp
 385 390 395

agg ttt gat gaa atg acc caa acc atg gac aaa ggg ttc ccg cag aga 1250
 Arg Phe Asp Glu Met Thr Gln Thr Met Asp Lys Gly Phe Pro Gln Arg
 400 405 410

gtg gta aaa cac ttt cct gga atc agt atc cgt gtt gat gct gct ttc 1298
 Val Val Lys His Phe Pro Gly Ile Ser Ile Arg Val Asp Ala Ala Phe
 415 420 425

cag tac aaa gga ttc ttc ttt ttc agc cgt gga tca acg caa ttt gaa 1346
 Gln Tyr Lys Gly Phe Phe Phe Phe Ser Arg Gly Ser Thr Gln Phe Glu
 430 435 440 445

tac gac att aag aca aag aat att acc cga atc atg aga act aat act 1394
 Tyr Asp Ile Lys Thr Lys Asn Ile Thr Arg Ile Met Arg Thr Asn Thr
 450 455 460

tgg ttt caa tgc aaa gaa cca aag aac tcc tca ttt ggt ttt gat atc 1442
 Trp Phe Gln Cys Lys Glu Pro Lys Asn Ser Ser Phe Gly Phe Asp Ile
 465 470 475

Fig. 2C

aac aag gaa aaa gca cat tca gga ggc ata aag ata ttg tat cat aag 1490
 Asn Lys Glu Lys Ala His Ser Gly Gly Ile Lys Ile Leu Tyr His Lys
 480 485 490

agt tta agc ttg ttt att ttt ggt att gtt cat ttg ctg aaa aac act 1538
 Ser Leu Ser Leu Phe Ile Phe Gly Ile Val His Leu Leu Lys Asn Thr
 495 500 505

tct att tat caa taaattcata gacctaaaat aaacctcaac aggtctttta 1590
 Ser Ile Tyr Gln
 510

atataaattc tgcttcaaaa tagaataaaa ccattcttta acaacaagtt gctggctcta 1650
 gttctaaata tccaaattca atggccattt tgagctgcct gattctttta ataggaagtt 1710
 attatgtaga aacaaaaatc tctgactgta cttaagcct atttcatgct ttgtggactt 1770
 ggagaagaca tgtcttataa ctgaatactg aaacatttat taaaccaatc tttagcattc 1830
 tg 1832

Fig. 2D

Leader Peptide		
1	M---K-----RLLLLFLFFITFSSAFPLVR---MM---E-----NEENVQL-AQAYLNQFYSLIEIGNHLVQSK-NPSLIDDKIREMQ	contig 355 long
1	HSFP-----P-.L.WGVV.HS.ATL---ET---QEQ-DV---D-.V.K.EKY.N.KND.RQVEKRR-.SGPWVE.LKQ..	contig 355 short
1	FSL-----T.PF.L.LHVOI.K...-V---SS---KEK-NT-----KT-V.D.EK.Q.PSNQYQSTRKN-GTNV.VE.LK...	COLL1HUM.PRO
1	HPGV-----LAAF...SWTH-CR.L..PS---GG---DED-DLS.DL.F-.ER..RSY.H-PTNLGILKEN-AA.SMTERL....	COLL2HUM.PRO
1	TV.CAV-CLLPGSLA.PL---PQ---AG-GMS.LQWEQ-.D..KR.LYDS.TKNA-----NSLEA.LK...	COLL3HUM.PRO
1	K-----F..IL.LQA.A.G.L..NS---ST-----SLEKN.LF-GER.EK..G..NKLPVTKM.YSGN.MKE..Q...	MATRUM.PRO
1	S.PI.L.LCVAVC..Y..DG---AA---RGE-DTS---MN-.V.K..ENV.D.KDKVKQF.RR.-DSGPVVK.....	METAHUM.PRO
1	M-----H.AF.V.LCLPVC..Y..SG---AA---KEE-DS---KD-.Q..EKY.N..KDKVKQF-RR.-DSN..VK..QG...	ST01HUM.PRO
1	APAAW-----LRSAAR.LLPPMLLL-----QPPPL.AR--A.PPDVH..HAERRGPQWHAALPSSP	ST02HUM.PRO
1	SPAPRPP-----RCLL.PLLTLGTALASLG---SAQSSFSPE.W.Q.YGY.PPGDLRTHTQR-SPQSLSAA.AA...	ST03HUM.PRO
1	GSDPSAPGRPGWTGS.LGDREEAARPL.PLLLV--LLGCLGLVAA.DAEVH.ENW.RLYGY.PQPSR.MSTM-RSAQILASALA...	MTM1HUM.PRO
1	ILLTFSTGRR---LD.VHSG-----VFFLQTLWLICATGTEQYFNEVW.QKYGY.PPTDPRMSVVR-SAETMQSALAA...	MTM2HUM.PRO
1	QQFGG-----LEA.G-----I-----DEATL-----	MTM3HUM.PRO
1	NCQQLWLG-----FLLP.TVSGRVLGLA.-----VAPVD..S.YGY.QKPLE--GSNFKPED.TEAL.AF.	MMP 17P
1	HPGV-----LAAF...SWTH-CR.L..PS---GG---DED-DLS.DL.F-.ER..RSY.H-PTNLGILKEN-AA.SMTERL....	MMP 18P
1	-----DPGTV-----	MMP 20P
1	GRGARVPS-----EAPGAGV.RRW.G.A--VALCL.PA---LVLLARLGAPAVPAW----	MMP 21P
1	EALMARGAL TGP.RA.C.LGCLL.H.AAAPS---PIIKFPGD-VAPKTDKE.-VQ...T..GCPK.SCN.-----FVLK.TLKK...	MMP 22P
1	SLWQPL---V.V.LVLGCC.AAPRQRS---TLVLFPGDLRT.LTDR..-EE..YRY-----GYTRVAEMRGESKSLGPALLL..	GELAHUM.PRO
		GELB HUM.PRO

Cystine switch		
68	AFEGLTVTGRLDSENTLEIMKTPRCGVPD-----VGQYG-----Y--TLPGWRKYNLTYRIINYT--PDMARAADVDEAIQEGLEVMSKVT	contig 355 long
68	-----	contig 355 short
69	E...K..KP.AE.KV.Q.....A.FV-----LTEGN.R.EQTH....E...LP.D.H..EKAFL..N..	COLL1HUM.PRO
68	R...N..KPNEE.DM.K.....S.GFM-----LTPGN.K.ERT.....R...QLSE.E.ER..KDAF.L..VAS	COLL2HUM.PRO
73	S....E...K.D.DV.K.....E.N-----VFPRTLK.S.M.....V....THSE.EK.FKAKF...D...	COLL3HUM.PRO

Fig. 3A

64	K...PI...M.N.RVI...QK.....AE.S-----LFPNS.K.TSKW.....VS.--R.LPHIT..RLVSKA.NM.G.EI	MATRHUM.PRO
69	H.L..K..Q..TS...M.HA.....HHFR-----EMPGG.V...HYI...N.....N.ED..Y..RKAFAQ..N..	METAHUM.PRO
69	K.L..E..K..D..V.RK.....HFR-----TFPGI.K..TH...V...LPKD..S.VEKA.K.EE..	STO1HUM.PRO
68	K.L..E..K..TD..V.RK.....HFS-----SFGPM.K..TH...V...LP.D..S..EKA.K.EE..	STO2HUM.PRO
60	---APAPATQEA PRPASSLRP.....PSDGLSA---RNQKRFVL SGG R.E.TD.....LRFPW---QLVQEQ.RQTMA.A.K..D..	STO3HUM.PRO
70	K.Y..Q...KA.AD.MKA.RR.....KFGAEIKANVRR--KR.AIQGLK.QHNEI.FC.Q...--KVGEY.TY...RKAFR..ESA.	MTM1HUM.PRO
88	R.Y.IP..V..EE.K.W..R.....QFGVRVKANLRRRRKR.AL.GRK.NNH..FS.Q...--EKLGWYHSM..VRRAFR..EQA.	MTM2HUM.PRO
78	Q.Y.INM..KV.R..IDW..K.....Q--TRGSSKFHRRKR.AL.GQK.QHKHI..S.K.V--KVGDPETRK..RRAF D..QN..	MTM3HUM.PRO
19	-----AL.....SL..LPVLTQ---ARRRQ-APAPTK.N.R..SW.VRTFPRDSPLGHTD.RALMYA.K...DIA	MMP 17P
62	EASE.P.S.Q..DA.RAR.RQ...LE.P-----FNQKTLK.LLLG-R..KH..F..L.LP--STLPPHTARA.LRQAFQD..N.A	MMP 18P
73	S...E..K..D..DV..K.....E.N-----VFPRTLK.S.M.....V.....THSE.EK.FKKAFAK...D..	MMP 20P
7	-----AT.RK...SL..VLGVAGL---VRRRRR.ALGSV.K.RT..W.VRSFPQSSQLSQET.RVLM SYA.MA.GMES	MMP 21P
49	-----SAAQG.VAA.GLSAV.PTR..GPLAP-----RRRRYTILTPARLR.DHL.....LSFPRNL-LSPRETRR.LAAAFRM..D.S	MMP 22P
79	K....PQ..D.Q..I.T.RK...N.....AN.N-----FFPRK.K.D.NQI.....G...LDPET..D.FARAFQ...D..	GELAHUM.PRO
76	KQLS.PE..E..A..KA.R.....L.RFQ-----TFEGDLK.HHH.I..W.Q..S--E.LP..VI.D.FARAFAL..A..	GELB HUM.PRO
143	PLKFTKI-----SKGIADIMIAFRTRVHGRC-----PRYFDGPLGLVGHAFPPGPG-LGGDTHFDEDENWKDGA-----	contig 355 long
143T...V-----E.Q...S.VRGD.RDN-----SP-.....G.N.A..Q...-I..A.....R..NNFR-----	contig 355 short
146I..R-----Q.E..N..YQ.D.DN-----SP-.....N.I.A..Q..Q..-I..A..AE.T..NTS-----	COLL1HUM.PRO
145N..RL-----HD.....S.GIKE.DF-----YP-.....S.L.A.....N-Y..A..D..T..SSSK-----	COLL2HUM.PRO
150H.R.V-----VW.T...G.ARG A.DS-----YP-.....GNT.A..A..T...A.....R..DGSSLGIN-----	COLL3HUM.PRO
141S.....NT.M...LVV.ARG A.DF-----HA...KG.I.A..G.S.-I..A.....F..THSG-----	MATRHUM.PRO
146T.SRL-----YE.E...S.AV.E.DF-----YP-.....GN..A..YA.....IN..A..D..Q...TT-----	METAHUM.PRO
146T.SRL-----YE.E...S.AVKE.DF-----YS-.....GHS.A..Y.....-Y..I..D..K..E.AS-----	STO1HUM.PRO
145T..E-----V---HE.R...D.ARYND.DD-----LP-.....G.I.A..F.KTHR-E..V..Y..T..IG--D-----	STO2HUM.PRO
142R.REVPYAYIREGHEKQ...F.AEGF.DS-----TP-.....EG.F.A..YF...N-I.....SA.P..VRNEDL-----	STO3HUM.PRO
156		MTM1HUM.PRO

Fig. 3B

176	V.QEVPYEDIRLRQKE	VL.ASGF.DS	SP	TG.F.A.YF	A.P.FSSTD	MTM2HUM.PRO
164	T.EEVPYSELENGK-RDV	P.I.ASGF.DS	SP	EG.F.A.YF	S.P.LGNPNH	MTM3HUM.PRO
88	N.HE	VA	GST	Q.D.SKAD.NDG	G.TVA.F.HHHTA	D.A.FRSSD
141	T.QEV	QA.A	RLS.HG.QSSY	SNT	GR.A.DI.EL	SV
150	N.RL	HD	S.GIKE.DF	YP	S.L.A	N.Y.A.D.T.SSSK
78	G.T.HE	VDSPQGP	L.D.ARAF.QDS	YP	LG.T.A.F.EHPIS	DE.T.FGSKA
126	FS.REVA	PEQPS	LR.G.YPIN.TD.LVSALHHC	T.E.A.F.PH	GI	DS.Y.VLGPTR
156	R.SR	HD.E	N.GRWE.DG	YP	KD.L.A.A.T.V	S.D.L.LGEGQVVRKYGNADG
153	T.RV	YSRD	V.Q.GVAE.DG	YP	KD.L.A	-IQ.A.D.L.SLKGWVPTFRGNADG
206						contig 355 long
263						contig 355 short
208						COLL1HUM.PRO
207						COLL2HUM.PRO
212						COLL3HUM.PRO
208	FLYA					MATRHUM.PRO
208						METAHUM.PRO
208						ST01HUM.PRO
207						ST02HUM.PRO
203						ST03HUM.PRO
228						MTM1HUM.PRO
248						MTM2HUM.PRO
235						MTM3HUM.PRO
152						MMP 17P
201					YR	MMP 18P
212						MMP 20P
145						MMP 21P

Fig. 3C

194	----	----	YSW----	MMP 22P
231	EYCKFPELFNGKEYNSCTD	GRSDGLWCSTTYNFEKDGKYGFCPHEALFTMGNAEGQCKPFRFQGTSDCTTEGRDGYRWCGTT		GELAHUM.PRO
228	AACHFPFI	FEGRSYSACTTDGRSDGLPWCSTTANYDTDDRFGFCPSERLYTRDGNADGKPCQFPFI	FQGSYSACTTDGRSDGYRWCAAT	GELBHUM.PRO
207	----	----	GFNLFLVAAHFGHAL	contig 355 long
164	----	----	----	contig 355 short
209	----	----	EY.HR.....L.S.	COLL1HUM.PRO
208	----	----	NY.....S.	COLL2HUM.PRO
213	----	----	Y.....S.	COLL3HUM.PRO
212	----	----T.L.L.S.	MATRHUM.PRO
209	----	----	T.....T.V.I.S.	METAHUM.PRO
209	----	----	T.....I.S.	STO1HUM.PRO
208	----	----	T.....L.S.	STO2HUM.PRO
204	----	----	DQ.TD.LQ.....V.	STO3HUM.PRO
229	----	----	N.NDI.....V.L....	MTM1HUM.PRO
249	----	----	H.N.....V.L....	MTM2HUM.PRO
236	----	----	D.ND.....V.L....	MTM3HUM.PRO
153	----	----	AH.MD.A.V.....I	MMP 17P
203	----	----	V.RII...V....	MMP 18P
213	----	----	Y.....S.	MMP 20P
146	----	----	SQGLE-----Q.LAGG-	MMP 21P
197	----	----	-----KKGW	MMP 22P
321	EDYDRDKKYGFCPETAMSTV	-GGNSEGAPCVFPFTFLGNKYESCTSAGRSDGKMWCAATTANYDDDRKMGFCPDQ.YS.	-----M	GELAHUM.PRO
318	ANYDRDKLFGFCPTRADSTVMGNSAGELCVFPFTFLGKEYSTCTSEGRDGRLLWCATTSNFSDSKKMGFCPDQ.YS.			GELBHUM.PRO

Fig. 3D

FIG. 3E

Zn++ binding domain		
223	GLSHNDQTALMFPNVVS-L-DPRKYPLS--QDDINGIQSIYGG-----LPKEPAKKEPTIP-----	contig 355 long
180	-----	contig 355 short
225	...T.IG...Y.S.-T-F--SGDVQ.A--...D.A..RSQNPVQ-----IG.QT-----	COLL1HUM.PRO
224	...A.S.PG...Y...-A-FRETSN.S.P--...D.A..LSSNPIQ-----TG.ST-----	COLL2HUM.PRO
229	...D.K.PG...I.-T-YTGKSHFM.P--D.VQ...L..PGDE-----DPN..H.KT-----	COLL3HUM.PRO
221	...MG.S.PN.V.Y.T.-G-NG..QNFK..--K..KL-----	MATRUM.PRO
225	...G.S.PK.V...T.K--YV.INTFR.--A..R...L..DPKENQRLP-----NPDNSE-----	MATRUM.PRO
225	...F..ANTE...Y.L.H.-.T.LTRFR..--L..PPDSPETP.VPTEPV.P..GT-----	STO1HUM.PRO
224	...F..ANTE...Y.L.N.-FTELAQFR..--V...L..PPASTEETP.VPTKSV.SGSEM-----	STO2HUM.PRO
222	...Q.TTAAK...SAF-----TFR...LSP..CR.V.HL.QP---WPTVTSRT-----	STO3HUM.PRO
246	...E.S.PS.I.A.F.Q--MM.TENFV.P--D..RR..QL..ESG-----FPTKM.PQ.-RT-SRPSVPDKPKNPT-----	MTM1HUM.PRO
266	...E..SNPN.I.A.F.Q--WK.VDNFK.P--E..LR..QL..TPDGQPQTQ.LPTVT.RR.GR.-DHRPPRPQPPPGGKPERPPKP-----	MTM2HUM.PRO
254	...E...P..I.A.F.Q--YME-QTLQ.P--N.YR--HQR.MSPDKIPPPTTR.LPTV..PHRS..-PADPRKNDRKP RPPTGRPSYP-----	MTM3HUM.PRO
171	...VAAHSI.R.Y.QGPVG..LR.G.PYE- KVR-VWQL..VRESVSPTAQ.E-----	MMP 17P
219	...G..RYSQ...A.V.EG---YRPHFK.H--P.VA...AL..KKSPVIRDEEEE.TEL.TV.PV.TEPS-----	MMP 18P
229	...D..K.PG...I.-T-YTGKSHFM.P--D.VQ...L..PGDE-----DPN..H.KT-----	MMP 20P
157	-----PVDEELGFS-----	MMP 21P
218	...M..QHGR...-----H.NATLRGWKALS..ELW.LHRL..C-----LDRLFVCASWARRGF-----	MMP 22P
410	...E..Q.PG...A.I.-T-YT--KNFR..--K..EL..ASPD---ID.GTG.TPTLG.VT-----	GELAHUM.PRO
408	...D..SVPE...Y.M.R--FTEGP--..H--K..V...RHL..PRPEPRPPTTTTPQ.TA.PTVCPTGPTVHPSERPTAGTGPSPA-----	GELBHM.PRO
277	-----HACD--PDLTFDAITTFREVMFFKGRHLWR-IYYDITDVE-FELIASFWPSLP---ADLQAAVENP-----	contig 355 long
234	-----	contig 355 short
276	...K...--SK.....I.G.....D.FYM..TNPFPYE..-LNF.SV..Q.---NG.E...FAD-----	COLL1HUM.PRO
277	...KP...--S.....L.G.IL...D.YF..-RHPQLQR..-MNF.SL.....TGI.....DFD-----	COLL2HUM.PRO
282	...DK...--S.SL....SL.G.T.I..D.FF..-LHPQQV.A.-LF.TK...E.---NRID....H.S-----	COLL3HUM.PRO
259	-----	MATRUM.PRO

Fig. 3E

FIG. 3F

280	-----AL.---N.S...V..VGNKIF...D.FF.L-KVSRPKTS-WN..S.L..T.---SGIE....IEA	METAHUM.PRO
288	-----AN.---A.S...VS.L.G.ILI..D.F.-KSLRKLEP.-LH..S.....SGVD....VTS	STO1HUM.PRO
287	-----AK.---A.S...S.L.G.YL..D.YF.-RSHWNEP.-H..SA.....SY.D....VNS	STO2HUM.PRO
269	-PALGPOAGIDTNEIAPLEDPDA--CEAS...VS.I.G.LF..AGFV..L-RGGQLQGYPA.ASRH.QG...SPVD..F.DAQ	STO3HUM.PRO
314	-----YGP-----NI.---GN--..TVAML.G.MFV..E.WF..VRNNQVM.GYPM-P..GQ..RG...SINT...RKD	MTM1HUM.PRO
351	GPPVQPRATERPDQYGP-----NI.---G--..TVAML.G.MFV...WF..VRHNRVL.NYPMP-.GH..RG...G.IS....RQD	MTM2HUM.PRO
334	GAK-----P-----NI.---GN--..NTLAIL...MFV..DQWF..VRNNRVM.GYPMQ-.TY..RG...PSID.V...SD	MTM3HUM.PRO
225	-PPLLPEPPDNRSSAPP--RKDVPHR--CSTH...VAQI.G.AF...KYF..LTRDRHLVSLQPAQMHR..RG..LHLDSDV.V..RTS	MMP 17P
285	-----MPDP.S--SE.D-AMMLGP.GKTYA...DYV.TVSDS---GPGPLFRVSAL.EG..GNLD--A.V.S-.R	MMP 18P
282	-----DK.---S.SL...SL.G.T.I..D.FF..LHPQQV.A.-LF.TK..E...NRID....H.S	MMP 20P
167	-----G-----RVN.L-----	MMP 21P
271	-----CDARRRLMKRLCP--SS..FCYEFP.PTVA.TPPPP-----TKTRLVPEGRNVTRFCG-----	MMP 22P
467	-----EI.K-Q-IV..G.AQI.G.IF...D.FI..TVTPRDKPMG-PL.V.T..E...EKID.V..A.Q	GELAHUM.PRO
492	GTPGPPTAGPSTATTVPVDD..N--VNI-...AEIGNQLYL..DGKY..FSEGRGRPQPGF...DK..A...--RK.DSVF.E.L	GELBHUM.PRO
342	<u>RDKTLVFKDENFWMIRGYAVLPDYPKSIHT-LGFPGRVKKIDAAVCDK-TTRKTYFFVGICWRFDEMTQIMDKGFPQRVVKHFFGISIR</u>	contig 355 long
294	contig 355 short
337	..EVRF..GNKY.AVQ.QN..HG...D.YSSF...RT..H...LSEE-N.G.....ANKY..Y.YKRS..P.Y.KMIAHD...GHK	COLL1HUM.PRO
338	..L.FL..GNQY.ALS..DI.QG...D.-SNY...SS.QA.....F---YRS.....NDQF..Y.NQR.F.EP.Y.KSISGA...ESK	COLL2HUM.PRO
343	H.L.FI.RGRK..ALN..DI.EG...K.-SE..L.KE...S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED...GDK	COLL3HUM.PRO
261	-----KRS-NS..K-----	MATRHUM.PRO
341	.NQVFL...DKY.L.SNLRPE.N.....S-F...NF.....FNP-RFYR.....DNQY..Y..RR.M..P.Y.KLIT.N.Q..GPK	METAHUM.PRO
349	K.LVFI..GNQ..A...NE.RAG..RG...-PT.R.....IS..-EKN.....EDKY.....KRNS.EP...KQIAED...DSK	STO1HUM.PRO
348	..TVFI..GNE..A...NE.QAG..RG...-PTIR.....S..-EKK.....AADKY.....NS.S.EQ...RLIADD...VEPK	STO2HUM.PRO
352	GH-WF.QGAQY.VYD.EKPLVG-.APL-.E..LVRF--VH..LVWGPEKN.I..R.RDY...HPS.RRV.SPV.R.ATD-WR.VPSE	STO3HUM.PRO
377	GKRVF-..GDKH.VFDEASLE.G...H.-KE..RGLPTD....LFWM-PNG.....R.NKYY..N.ELRAV.SEY.KNIKV-WE..PES	MTM1HUM.PRO
428	GRFVF-..GDRY.LF.EANLE.G..QPL-.SY.LGIPYDR..T.IWWE-P.GH.F..QEDRY...N.E..RG.P.Y.KPISV-WQ..PAS	MTM2HUM.PRO
398	GNFVF-..GNKY.VFKDTTLQ.G..HDL-IT..SGIPPHG..S.IWWE-DVG.....K.DRY..YS.EMK...P.Y.KPITV-WK...PES	MTM3HUM.PRO

Fig. 3F

310	DH..VF..GDRY.VFKDNN.EEG..RPV-SDFSL.PGG--...FSWA-HNDR...KDQLY..Y.DH.RH..P.Y.AQSPL-WR.VPST	MMP 17P
356	TQW.HF..GDKV.RYINFKMS.GF..KLN-----RSEPNL...LYW-PLNQ.VFL.K.SGY.QW..LAR.DFSSY.KPIKGL.T.VPNQ	MMP 18P
343	H.L.FI.RGRK..ALN..DI.EG..K.-SE..I.KE...S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED....GDK	MMP 20P
174	-----	
323	-Q...HK.GKVV..-----KDQPLEFSY..-----YLALGEA.LSI.ANA	MMP 21P
529	EE.AVF.AGNEY.IYSASTLERG...PL-.S..L.PD.QRV...FNWS-KNK...I.A.DKF..YN.VKKK..P...KLIADAWNA.PDN	MMP 22P
576	SK.LFF.SGRQV.VYT.AS..G--.RRLD-K..LGAD.AQVTG.LR-S-GRG.MLL.S.RRL...VKA.MV.PRSASE.DRM...VPLD	GELAHUM.PRO
		GELBHAM.PRO
425	VDAAFQYK--GFF-----FFSRGSTQFEYDIKTKNITRIMRTNT-----WFQCKEP-----KN	contig 355 long
382	-----	contig 355 short
426	V...MKD...-----Y.FH.TR.YKF.P...R.LTLQA.S-----N.RKN	COLL1HUM.PRO
424	V...QKEH...-----HVES.PRYAF.LIAQRV..VA.G.K-----LN.RYG	COLL2HUM.PRO
431	VY--EKN.YI-----Y.FN.PI....S.WSNR.V.V.PA.S-----ILW.	COLL3HUM.PRO
267		MATRHUM.PRO
429	I..V.-SKNKYY-----Y.FQ..N.....FLLQR..KTLKS.S-----G.	METAHUM.PRO
437	I..V.-EEF...-----Y.FT..S.L.F.PVA.KV.HTLKS.S-----LN.	STO1HUM.PRO
436	VL--QAF...-----Y.FS..S...F.PNARMV.H.LKS.S-----LH.	STO2HUM.PRO
436	I.....DADGY-----AY.L..RLYWK.F.PVKYKALE-GFPRLVGPDF.G.A..ANTLL	STO3HUM.PRO
463	PRGS.MGSDEV.-----TY.YK.NKYWKFNQKL-KVEPGYPKSALRD.MG.-----PSGGRP-----DEGTEETEVIIEVDEEG	MTM1HUM.PRO
514	PKG..LSNDAAY-----TY.YK.TKYWK.F.NERL-RMEPGYPKSILRDFMG.Q.HVEPGRPWDVARPPFNPHGGAEPGADSAEGDVGDGD	MTM2HUM.PRO
484	PQG..VH.EN...-----TY.YKEGVL-.IQITRYSRLEPGHPRSTLKDL.SG.D---GPTDRVKEGHSP-----DDVD---	MTM3HUM.PRO
395	L.D.MRWSDGA-----SY.F..QEYWKVLDGELEVAP-GYPQSTARD.LV.GDSQADGS-----VAAGVDAAEGRAPPGQHDQSR	MMP 17P
429	PS..MSWQDG-----RVY.FK.KVYWRLN-QQLRVEKGYPRNISHN.MH.RPRTIDTTPSGGNTTPS-----	MMP 18P
431	...VY--EKN.YI-----Y.FN.PI....S.WSNR.V.V.PA.S-----ILW.	MMP 20P
175	-----	MMP 21P
363	N-----EGTYTC-----VVRQRQRLTTYSMRVRVRG	MMP 22P
617	L..WDLQGG.HS-----Y.FK.AYYLKENQSLKSVKFGSTKS--D.LG.	GELAHUM.PRO

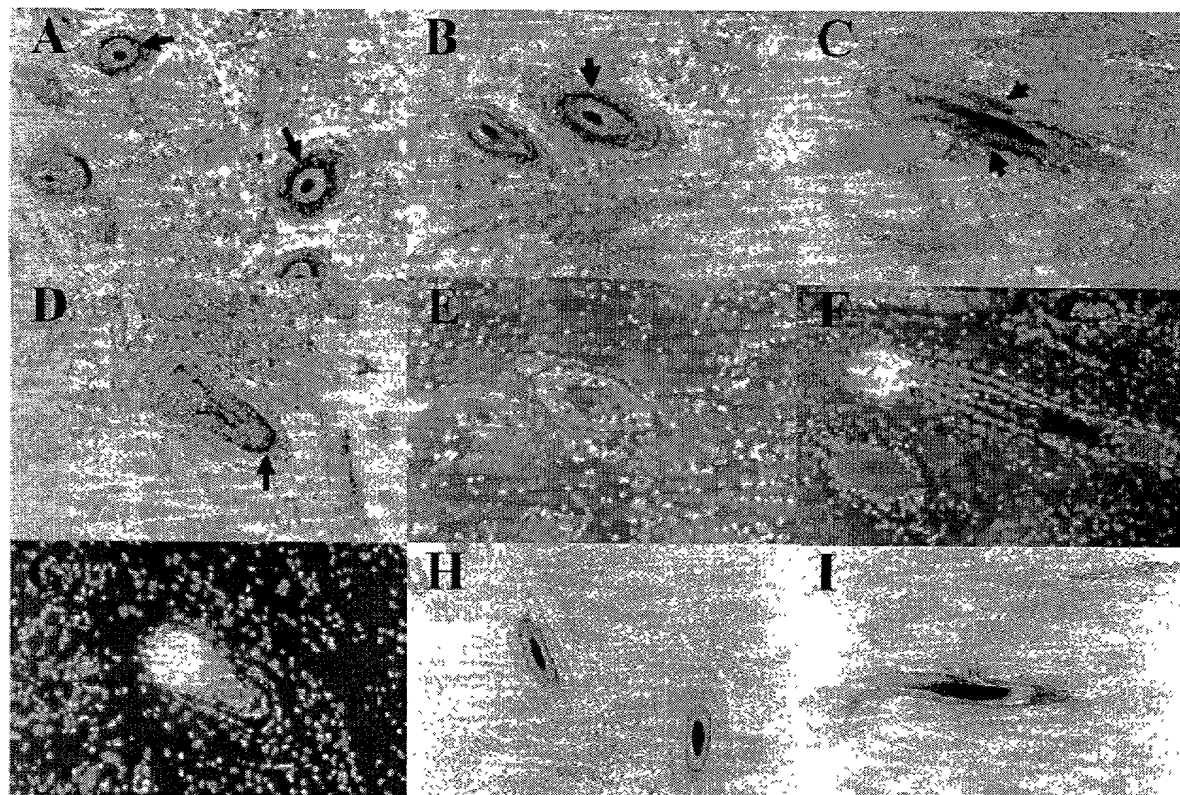
Fig. 3G

661	THDV...REKAY.CQDR.YW.V.SRS.LN---- <td>GELBHUM.PRO</td>	GELBHUM.PRO
471	SSFGFDINKEKAHSGGIK-----ILYHKSLSFI---FGIVHLLKNTS----IYQ	contig 355 long
428	contig 355 short
426		COLL1HUM.PRO
424		COLL2HUM.PRO
431		COLL3HUM.PRO
267		MATRHUM.PRO
429		METAHUM.PRO
437		ST01HUM.PRO
436		ST02HUM.PRO
536	GG-----AVSAAAVLPVL.L.LVLAVGLAVFFRRHGTPrRL.L.C.RSLLDKV	ST03HUM.PRO
599	GD..AGV..DGGSRVVQMEEVARTVNVVMV.VPLL.L.CVLGLTYAL.QMQRKGAPRVLL.CKRSQEW	MTM1HUM.PRO
548	-----IV..LDNTASTVKAIA.VIPCI.A.CLLVLVTVFQFKRKGTPRHIL.CKRSMQEW	MTM2HUM.PRO
470	.ED.YEVCSTS-----GASSPPGAPG.VAATML.LLPPL-----PGALWTAQAALT--L	MTM3HUM.PRO
488	-----GT..TLDTTLSATETT-----FEY	MMP 17P
175		MMP 18P
363		MMP 20P
617		MMP 21P
661		MMP 22P
		GELAHUM.PRO
		GELBHUM.PRO

Fig. 3H

stimulated PBL
fetal skin
cartilage
adipose tissue
bone
PBL
ovary
umbilical cord
parotid
thyroid
salivary gland
pancreas
adrenal gland
placenta
spinal cord
fetal liver
fetal brain
cerebellum
brain
trachea
lung
liver
kidney
skin
thymus
stomach
spleen
sm. intestine
colon
bone marrow
uterus
testis
skel. muscle
prostate
mammary gland
heart

Fig. 4



A-G: Antisense RNA probe for human MMP 25

H and I: Sense RNA probe for human MMP 25

Arrows in A, B, C, and D highlight cells in the hair follicle that express MMP 25 message

Cell nuclei are counterstained with H33258 in E, F, and G.

Fig. 5